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Specificity of restriction endonucleases and DNA modification methyltransferases – a review (Edition 3)*

(Recombinant DNA; isomers; iso/hetero-schizomers; iso/hetero-hypekomers; iso/hetero-prostomers; palindromes; relaxed sequence specificities; cleavage positions; methylation sensitivities; novel sequence specificities)

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* Dedicated to Dr. Felice A. de Jong

Abbreviations: Ad, adenovirus; AdoMet, *S*-adenosylmethionine; bp, base pair(s); ds, double strand(ed); DNase, deoxyribonuclease; ENase, restriction endonuclease; MTase (M·), DNA modification methyltransferase; nd, not determined; nt, (deoxy)nucleotide(s); PolIk, Klenow (large) fragment of *E. coli* DNA polymerase I; ss, single strand(ed); SV, simian virus; T4DNALig, T4 DNA ligase; wt, wild type.
See also INTRODUCTION, sections (**a**–**e**), pp. 4–8, and Table II, **Footnotes** (**a**)–(**j**), pp. 125–128).

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SUMMARY

The properties and sources of all known class-I, class-II and class-III restriction endonucleases (ENases) and DNA modification methyltransferases (MTases) are listed and newly subclassified according to their sequence specificity. In addition, the enzymes are distinguished in a novel manner according to sequence specificity, cleavage position and methylation sensitivity. Furthermore, new nomenclature rules are proposed for unambiguously defined enzyme names.